

Claims:

1. A high throughput integrated system for qualitative and quantitative biomolecules analysis comprising;
 - a) a robotic platform fitted with multiple, spatially arrayed affinity microcolumns,
 - b) a mass spectrometer target having a spatial array corresponding to the same spatial array as the affinity microcolumns, and,
 - c) a mass spectrometer capable of accepting the spatially arrayed target.
2. The system of Claim 1 wherein the spatial array comprises between 4 and 1536 elements.
3. The system of Claim 1 wherein the robotic platform further comprises multiple processing stages.
4. The system of Claim 1 wherein if the affinity microcolumns receive specific biological molecules in a biological media, the specific biological molecules are retrieved via affinity interaction.
5. The system of Claim 1 wherein the mass spectrometer target has modifying activity.
6. The system of Claim 1 wherein the mass spectrometer is a matrix-assisted laser desorption/ionization time-of-flight mass spectrometer.
7. The system of Claim 3 wherein at least one of the multiple processing stages is for the selective isolation of specific biological molecules present in a biological media using affinity microcolumns.
8. The system of Claim 3 wherein at least one of the multiple processing stages is for rinsing the affinity microcolumns free of non-specifically retained compounds.
9. The system of Claim 3 wherein at least one of the multiple processing stages is for the deposition of selectively retained biological molecules onto a mass spectrometer target.
10. The system of Claim 1 wherein if multiple different samples of biological media are presented, then they are processed relatively simultaneously and in parallel

using the robotic platform fitted with multiple, spatially arrayed affinity microcolumns and the mass spectrometer target having a spatial array corresponding to the same spatial array as the affinity microcolumns.

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